

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/570,011  
Source: IFWP  
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# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 03/08/2006

PATENT APPLICATION: US/10/570,011

TIME: 13:16:18

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\03072006\J570011.raw

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3 <110> APPLICANT: Kureha Chemical Industry Company, Limited
4     KAMATA, Toru
5     MITSUSHITA, Junji
7 <120> TITLE OF INVENTION: Antibodies to Nox1 polypeptide, method for the detection of
cancer using
8     Nox1 gene and method for screening substances suppressing cancer growth
10 <130> FILE REFERENCE: 0701012WO1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/570,011
C--> 12 <141> CURRENT FILING DATE: 2006-03-01
12 <160> NUMBER OF SEQ ID NOS: 27
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1734
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (71)..(1618)
24 <223> OTHER INFORMATION: Human Nox1 polypeptide of SEQ NO:2
27 <400> SEQUENCE: 1
28 ggacctctcc agaatccgga ttgctgaatc ttccctgttg cctagaaggg ctccaaacca      60
30 cctcttgaca atg gga aac tgg gtg gtt aac cac tgg ttt tca gtt ttg      109
31     Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu
32         1             5             10
34 ttt ctg gtt gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc      157
35 Phe Leu Val Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala
36     15             20             25
38 ttc ctg aaa tat gag aag gcc gac aaa tac tac tac aca aga aaa atc      205
39 Phe Leu Lys Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile
40 30             35             40             45
42 ctt ggg tca aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat      253
43 Leu Gly Ser Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn
44         50             55             60
46 ttt aac agc acg ctg atc ctg ctt cct gtg tgt cgc aat ctg ctg tcc      301
47 Phe Asn Ser Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser
48         65             70             75
50 ttc ctg agg ggc acc tgc tca ttt tgc agc cgc aca ctg aga aag caa      349
51 Phe Leu Arg Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln
52     80             85             90
54 ttg gat cac aac ctc acc ttc cac aag ctg gtg gcc tat atg atc tgc      397
55 Leu Asp His Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys
56     95             100             105
58 cta cat aca gct att cac atc att gca cac ctg ttt aac ttt gac tgc      445
59 Leu His Thr Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys

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60	110		115		120		125										
62	tat	agc	aga	agc	cga	cag	gcc	aca	gat	ggc	tcc	ctt	gcc	tcc	att	ctc	493
63	Tyr	Ser	Arg	Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	Ala	Ser	Ile	Leu	
64					130		135		140								
66	tcc	agc	cta	tct	cat	gat	gag	aaa	aag	ggg	ggg	tct	tgg	cta	aat	ccc	541
67	Ser	Ser	Leu	Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	Trp	Leu	Asn	Pro	
68					145		150		155								
70	atc	cag	tcc	cga	aac	acg	aca	gtg	gag	tat	gtg	aca	ttc	acc	agc	att	589
71	Ile	Gln	Ser	Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	Phe	Thr	Ser	Ile	
72					160		165		170								
74	gct	ggg	ctc	act	gga	gtg	atc	atg	aca	ata	gcc	ttg	att	ctc	atg	gta	637
75	Ala	Gly	Leu	Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	Ile	Leu	Met	Val	
76					175		180		185								
78	act	tca	gct	act	gag	ttc	atc	cgg	agg	agt	tat	ttt	gaa	gtc	ttc	tgg	685
79	Thr	Ser	Ala	Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	Glu	Val	Phe	Trp	
80	190				195		200		205								
82	tat	act	cac	cac	ctt	ttt	atc	ttc	tat	atc	ctt	ggc	tta	ggg	att	cac	733
83	Tyr	Thr	His	His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	Leu	Gly	Ile	His	
84					210		215		220								
86	ggc	att	ggg	gga	att	gtc	cgg	ggg	caa	aca	gag	gag	agc	atg	aat	gag	781
87	Gly	Ile	Gly	Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	Ser	Met	Asn	Glu	
88					225		230		235								
90	agt	cat	cct	cgc	aag	tgt	gca	gag	tct	ttt	gag	atg	tgg	gat	gat	cgt	829
91	Ser	His	Pro	Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	Trp	Asp	Asp	Arg	
92					240		245		250								
94	gac	tcc	cac	tgt	agg	cgc	cct	aag	ttt	gaa	ggg	cat	ccc	cct	gag	tct	877
95	Asp	Ser	His	Cys	Arg	Arg	Pro	Lys	Phe	Glu	Gly	His	Pro	Pro	Glu	Ser	
96					255		260		265								
98	tgg	aag	tgg	atc	ctt	gca	ccg	gtc	att	ctt	tat	atc	tgt	gaa	agg	atc	925
99	Trp	Lys	Trp	Ile	Leu	Ala	Pro	Val	Ile	Leu	Tyr	Ile	Cys	Glu	Arg	Ile	
100	270				275		280		285								
102	ctc	cgg	ttt	tac	cgc	tcc	cag	cag	aag	gtt	gtg	att	acc	aag	gtt	gtt	973
103	Leu	Arg	Phe	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	Thr	Lys	Val	Val	
104					290		295		300								
106	atg	cac	cca	tcc	aaa	gtt	ttg	gaa	ttg	cag	atg	aac	aag	cgt	ggc	ttc	1021
107	Met	His	Pro	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	Lys	Arg	Gly	Phe	
108					305		310		315								
110	agc	atg	gaa	gtg	ggg	cag	tat	atc	ttt	gtt	aat	tgc	ccc	tca	atc	tct	1069
111	Ser	Met	Glu	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	Pro	Ser	Ile	Ser	
112					320		325		330								
114	ctc	ctg	gaa	tgg	cat	cct	ttt	act	ttg	acc	tct	gct	cca	gag	gaa	gat	1117
115	Leu	Leu	Glu	Trp	His	Pro	Phe	Thr	Leu	Thr	Ser	Ala	Pro	Glu	Glu	Asp	
116					335		340		345								
118	ttc	ttc	tcc	att	cat	atc	cga	gca	gca	ggg	gac	tgg	aca	gaa	aat	ctc	1165
119	Phe	Phe	Ser	Ile	His	Ile	Arg	Ala	Ala	Gly	Asp	Trp	Thr	Glu	Asn	Leu	
120	350				355		360		365								
122	ata	agg	gct	ttc	gaa	caa	caa	tat	tca	cca	att	ccc	agg	att	gaa	gtg	1213
123	Ile	Arg	Ala	Phe	Glu	Gln	Gln	Tyr	Ser	Pro	Ile	Pro	Arg	Ile	Glu	Val	
124					370		375		380								

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126 gat ggt ccc ttt ggc aca gcc agt gag gat gtt ttc cag tat gaa gtg      1261
127 Asp Gly Pro Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val
128          385          390          395
130 gct gtg ctg gtt gga gca gga att ggg gtc acc ccc ttt gct tct atc      1309
131 Ala Val Leu Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile
132          400          405          410
134 ttg aaa tcc atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa      1357
135 Leu Lys Ser Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys
136          415          420          425
138 aca aaa aag gtt ggt cat gca gca tta aac ttt gac aag gcc act gac      1405
139 Thr Lys Lys Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp
140 430          435          440          445
142 atc gtg aca ggt ctg aaa cag aaa acc tcc ttt ggg aga cca atg tgg      1453
143 Ile Val Thr Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp
144          450          455          460
146 gac aat gag ttt tct aca ata gct acc tcc cac ccc aag tct gta gtg      1501
147 Asp Asn Glu Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val
148          465          470          475
150 gga gtt ttc tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa      1549
151 Gly Val Phe Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys
152          480          485          490
154 tgc tgt cac cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac      1597
155 Cys Cys His Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr
156          495          500          505
158 ttc aac aaa gaa aat ttt tga gttataggaa taaggacggt aatctgcatt      1648
159 Phe Asn Lys Glu Asn Phe
160 510          515
162 ttgtctcttt gtatcttcag taatttactt ggtctcgtca ggtttgagca gtcactttag      1708
164 gataagaatg tgcctctcaa gccttg      1734
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 515
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 2
174 Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
175 1          5          10          15
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179          20          25          30
182 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
183          35          40          45
186 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
187          50          55          60
190 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Ser Phe Leu Arg
191 65          70          75          80
194 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
195          85          90          95
198 Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
199          100          105          110
202 Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg

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203          115          120          125
206 Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
207          130          135          140
210 Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
211 145          150          155          160
214 Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Ile Ala Gly Leu
215          165          170          175
218 Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
219          180          185          190
222 Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
223          195          200          205
226 His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
227          210          215          220
230 Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
231 225          230          235          240
234 Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
235          245          250          255
238 Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
239          260          265          270
242 Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
243          275          280          285
246 Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
247          290          295          300
250 Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
251 305          310          315          320
254 Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
255          325          330          335
258 Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
259          340          345          350
262 Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
263          355          360          365
266 Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
267          370          375          380
270 Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
271 385          390          395          400
274 Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
275          405          410          415
278 Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
279          420          425          430
282 Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
283          435          440          445
286 Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
287          450          455          460
290 Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
291 465          470          475          480
294 Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
295          485          490          495
298 Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
299          500          505          510

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302 Glu Asn Phe
303      515
306 <210> SEQ ID NO: 3
307 <211> LENGTH: 2577
308 <212> TYPE: DNA
309 <213> ORGANISM: Rattus norvegicus
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (128)..(1819)
314 <223> OTHER INFORMATION: Rat Nox1 polypeptide of SEQ NO:4
317 <400> SEQUENCE: 3
318 ttctgagtag gtgtgcattt gagtgtcata aagacatata tcttgagcta gacagaagtt      60
320 cctatcctga aggatcccat cagagaaacc agattgctcc taagaggctc cagacctcca      120
322 tttgaca atg gga aac tgg ctg gtt aac cac tgg ctg tca gtt ttg ttt      169
323      Met Gly Asn Trp Leu Val Asn His Trp Leu Ser Val Leu Phe
324      1          5          10
326 ctg gtt tct tgg ttg ggg ctg aac att ttt ctg ttt gtg tac gtc ttc      217
327 Leu Val Ser Trp Leu Gly Leu Asn Ile Phe Leu Phe Val Tyr Val Phe
328 15          20          25          30
330 ctg aat tat gag aag tct gac aag tac tat tac acg aga gaa att ctc      265
331 Leu Asn Tyr Glu Lys Ser Asp Lys Tyr Tyr Tyr Thr Arg Glu Ile Leu
332          35          40          45
334 gga act gcc ttg gcc ttg gcc aga gca tct gct ttg tgc ctg aat ttt      313
335 Gly Thr Ala Leu Ala Leu Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe
336          50          55          60
338 aac agc atg gtg atc ctg att cct gtg tgt cga aat ctg ctc tcc ttc      361
339 Asn Ser Met Val Ile Leu Ile Pro Val Cys Arg Asn Leu Leu Ser Phe
340          65          70          75
342 ctg agg ggc acc tgc tca ttt tgc aac cac acg ctg aga aag cca ttg      409
343 Leu Arg Gly Thr Cys Ser Phe Cys Asn His Thr Leu Arg Lys Pro Leu
344          80          85          90
346 gat cac aac ctc acc ttc cat aag ctg gtg gca tat atg atc tgc ata      457
347 Asp His Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Ile
348 95          100          105          110
350 ttc aca gct att cat atc att gca cat cta ttt aac ttt gaa cgc tac      505
351 Phe Thr Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Glu Arg Tyr
352          115          120          125
354 agt aga agc caa cag gcc atg gat gga tct ctt gcc tct gtt ctc tcc      553
355 Ser Arg Ser Gln Gln Ala Met Asp Gly Ser Leu Ala Ser Val Leu Ser
356          130          135          140
358 agc cta ttc cat ccc gag aaa gaa gat tct tgg cta aat ccc atc cag      601
359 Ser Leu Phe His Pro Glu Lys Glu Asp Ser Trp Leu Asn Pro Ile Gln
360          145          150          155
362 tct cca aac gtg aca gtg atg tat gca gca ttt acc agt att gct ggc      649
363 Ser Pro Asn Val Thr Val Met Tyr Ala Ala Phe Thr Ser Ile Ala Gly
364          160          165          170
366 ctt act gga gtg gtc gcc act gtg gct ttg gtt ctc atg gta act tca      697
367 Leu Thr Gly Val Val Ala Thr Val Ala Leu Val Leu Met Val Thr Ser
368 175          180          185          190

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date